

CLAIMS

What is claimed is:

1. An isolated polynucleotide comprising a nucleotide sequence encoding a first polypeptide of at least 240 amino acids that has at least 80% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of arginyl-tRNA synthetase polypeptides of SEQ ID NOs:2, 4, 6 and 8,  
or an isolated polynucleotide comprising the complement of the nucleotide sequence.
2. The isolated polynucleotide of Claim 1, wherein the isolated nucleotide sequence consists of a nucleic acid sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, and 7 that codes for the polypeptide selected from the group consisting of SEQ ID NOs:2, 4, 6, and 8.
3. The isolated polynucleotide of Claim 1 wherein the nucleotide sequence is DNA.
4. The isolated polynucleotide of Claim 1 wherein the nucleotide sequence is RNA.
5. A chimeric gene comprising the isolated polynucleotide of Claim 1 operably linked to suitable regulatory sequences.
6. An isolated host cell comprising the chimeric gene of Claim 5.
7. An isolated host cell comprising an isolated polynucleotide of Claim 1.
8. The isolated host cell of Claim 7 wherein the isolated host is selected from the group consisting of yeast, bacteria, plant, and virus.
9. A virus comprising the isolated polynucleotide of Claim 1.
10. A polypeptide of at least 240 amino acids that has at least 80% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NO:2, 4, 6 and 8.
11. An isolated polynucleotide comprising a nucleotide sequence encoding a first polypeptide of at least 205 amino acids that has at least 90% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of glutamyl-tRNA synthetase polypeptides of SEQ ID NOs:10, 12 and 14,  
or an isolated polynucleotide comprising the complement of the nucleotide sequence.
12. The isolated polynucleotide of Claim 11, wherein the isolated nucleotide sequence consists of a nucleic acid sequence selected from the group consisting of SEQ ID NOs:9, 11 and 13 that codes for the polypeptide selected from the group consisting of SEQ ID NOs:10, 12 and 14.
13. The isolated polynucleotide of Claim 11 wherein the isolated polynucleotide is DNA.
14. The isolated polynucleotide of Claim 11 wherein the isolated polynucleotide is RNA.

15. A chimeric gene comprising the isolated polynucleotide of Claim 11 operably linked to suitable regulatory sequences.

16. An isolated host cell comprising the chimeric gene of Claim 15.

17. An isolated host cell comprising an isolated polynucleotide of Claim 11.

5 18. The isolated host cell of Claim 17 wherein the isolated host selected from the group consisting of yeast, bacteria, plant, and virus.

19. A virus comprising the isolated polynucleotide of Claim 11.

10 20. A polypeptide of at least 205 amino acids that has at least 90% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of a glutamyl-tRNA synthetase polypeptide of SEQ ID NOs:10, 12 and 14.

21. An isolated polynucleotide comprising a nucleotide sequence encoding a first polypeptide of at least 79 amino acids that has at least 80% identity based on the Clustal method of alignment when compared to a glutamyl-tRNA synthetase polypeptide of SEQ ID NO:16,

15 or an isolated polynucleotide comprising the complement of the nucleotide sequence.

22. The isolated polynucleotide of Claim 21, wherein the isolated nucleotide sequence consists of a nucleic acid sequence of SEQ ID NO:15 that codes for the polypeptide of SEQ ID NO:16.

20 23. The isolated polynucleotide of Claim 21 wherein the isolated polynucleotide is DNA.

24. The isolated polynucleotide of Claim 21 wherein the isolated polynucleotide is RNA.

25 25. A chimeric gene comprising the isolated polynucleotide of Claim 21 operably linked to suitable regulatory sequences.

26. An isolated host cell comprising the chimeric gene of Claim 25.

27. An isolated host cell comprising an isolated polynucleotide of Claim 21.

28. The isolated host cell of Claim 27 wherein the isolated host is selected from the group consisting of yeast, bacteria, plant, and virus.

30 29. A virus comprising the isolated polynucleotide of Claim 21.

30. A polypeptide of at least 79 amino acids that has at least 80% identity based on the Clustal method of alignment when compared to a glutamyl-tRNA synthetase polypeptide of SEQ ID NO:16.

35 31. An isolated polynucleotide comprising a nucleotide sequence encoding a first polypeptide of at least 243 amino acids that has at least 90% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of histidyl-tRNA synthetase polypeptides of SEQ ID NO:s18, 20 and 22,

or an isolated polynucleotide comprising the complement of the nucleotide sequence.

32. The isolated polynucleotide of Claim 31, wherein the isolated nucleotide sequence consists of a nucleic acid sequence selected from the group consisting of SEQ ID NOs:17, 19 and 21 that codes for the polypeptide selected from the group consisting of SEQ ID NOs:18, 20 and 22.

33. The isolated polynucleotide of Claim 31 wherein the isolated polynucleotide is DNA.

34. The isolated polynucleotide of Claim 31 wherein the isolated polynucleotide is RNA.

35. A chimeric gene comprising the isolated polynucleotide of Claim 31 operably linked to suitable regulatory sequences.

36. An isolated host cell comprising the chimeric gene of Claim 35.

37. An isolated host cell comprising an isolated polynucleotide of Claim 31.

38. The isolated host cell of Claim 37 wherein the isolated host is selected from the group consisting of yeast, bacteria, plant, and virus.

39. A virus comprising the isolated polynucleotide of Claim 31.

40. A polypeptide of at least 243 amino acids that has at least 90% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of histidyl-tRNA synthetase polypeptides of SEQ ID NOs:18, 20 and 22.

41. A method of selecting an isolated polynucleotide that affects the level of expression of an aminoacyl-tRNA synthetase polypeptide in a plant cell, the method comprising the steps of:

(a) constructing an isolated polynucleotide comprising a nucleotide sequence of at least one of 30 contiguous nucleotides derived from a nucleotide sequence selected from the group consisting of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37 and the complement of such nucleotide sequences;

(b) introducing the isolated polynucleotide into a plant cell; and

(c) measuring the level of an aminoacyl t-RNA synthetase polypeptide in the plant cell containing the polynucleotide.

42. The method of Claim 41 wherein the isolated polynucleotide consists of a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35 and 37 that codes for the polypeptide selected from the group consisting of SEQ ID NOs:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36 and 38.

43. A method of selecting an isolated polynucleotide that affects the level of expression of an aminoacyl-tRNA synthetase polypeptide in a plant cell, the method comprising the steps of:

(a) constructing an isolated polynucleotide of any of Claims 1, 11, 21 or 31;  
 (b) introducing the isolated polynucleotide into a plant cell;  
 (c) measuring the level of an aminoacyl-tRNA synthetase polypeptide in the plant cell containing the polynucleotide; and

5 (d) comparing the level of aminoacyl-tRNA synthetase polypeptide in the plant cell containing the isolated polynucleotide with the level of aminoacyl-tRNA synthetase polypeptide in a plant cell that does not contain the polynucleotide.

44. A method of obtaining a nucleic acid fragment encoding a aminoacyl-tRNA synthetase polypeptide comprising the steps of:

10 (a) synthesizing an oligonucleotide primer comprising a nucleotide sequence of at least one of 30 contiguous nucleotides derived from a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37 and the complement of such nucleotide sequences; and

(b) amplifying a nucleic acid sequence using the oligonucleotide primer.

15 45. A method of obtaining a nucleic acid fragment encoding the amino acid sequence encoding a aminoacyl-tRNA synthetase polypeptide comprising the steps of:

(a) probing a cDNA or genomic library with an isolated polynucleotide comprising a nucleotide sequence of at least one of 30 contiguous nucleotides derived from a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7, 9, 11,  
 20 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37 and the complement of such nucleotide sequences;

(b) identifying a DNA clone that hybridizes with the isolated polynucleotide;

(c) isolating the identified DNA clone; and

(d) sequencing the cDNA or genomic fragment that comprises the isolated DNA  
 25 clone.

46. A method for evaluating at least one compound for its ability to inhibit the activity of a aminoacyl-tRNA synthetase, the method comprising the steps of:

(a) transforming a host cell with a chimeric gene comprising a nucleic acid fragment encoding a aminoacyl-tRNA synthetase, operably linked to suitable regulatory  
 30 sequences;

(b) growing the transformed host cell under conditions that are suitable for expression of the chimeric gene wherein expression of the chimeric gene results in production of the aminoacyl-tRNA synthetase encoded by the operably linked nucleic acid fragment in the transformed host cell;

35 (c) optionally purifying the aminoacyl-tRNA synthetase expressed by the transformed host cell;

(d) treating the aminoacyl-tRNA synthetase with a compound to be tested; and

(e) determining the activity of the aminoacyl-tRNA synthetase that has been treated with a test compound.

47. A composition comprising an isolated polynucleotide of Claim 1.

48. A composition comprising an isolated polynucleotide of Claim 11.

5 49. A composition comprising an isolated polynucleotide of Claim 21.

50. A composition comprising an isolated polynucleotide of Claim 31.

51. A composition comprising a polypeptide of Claim 10, Claim 20, Claim 30, or Claim 40.

10 52. An isolated polynucleotide comprising the nucleotide sequence comprising at least one of 30 contiguous nucleotides of nucleic acid sequences selected from the group consisting of SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37 and the complement of such sequences.

53. An expression cassette comprising an isolated polynucleotide of Claim 1, Claim 11, Claim 21, or Claim 31 operably linked to a promoter.

15 54. A method for positive selection of a transformed cell comprising:

(a) transforming a plant cell with an expression cassette of Claim 53; and

(b) growing the transformed plant cell under conditions allowing expression of the polynucleotide in an amount sufficient to complement an amino-acyl t-RNA synthesis auxotroph in a plant cell to provide a positive selection means.

20 55. A method for positive selection of a transformed cell comprising:

(a) transforming a plant cell with a chimeric gene of Claim 5, Claim 15, Claim 25 or Claim 35; and

(b) growing the transformed plant cell under conditions allowing expression of the polynucleotide in an amount sufficient to complement an amino-acyl t-RNA synthesis auxotroph in a plant cell to provide a positive selection means.

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56. The method of Claim 54 wherein the plant cell is a monocot.

57. The method of Claim 56 wherein the plant cell is a dicot.